

## REMARKS

Applicants acknowledge election of Group II (claims 3, 6, 14, 15, 25, and 28) without traverse for examination purposes. Applicants have amended the specification and claims 3, 6, 14, 15, 25, and 28. The amendments to the specification and claims are shown in the attached Appendix. These amendments do not add new subject matter. In particular, the amendments to claims 3, 6, 14, 15, 25, and 28 are supported by the specification as noted below. Claims 1-33 are pending.

### Disclosure Objections

The Examiner objected to the disclosure as allegedly having informalities. Specifically, the Examiner notes that the brief description of Figures 3A, 3B, 3C, 3D, 10, 11, and 12 is insufficient for not being separately described. (Paper No. 9 at pages 6-7). Applicants have amended the specification to provide a brief description for each of those Figures. The Examiner also objected to the disclosure as allegedly not being double-spaced or at least 1.5 spaced with specific reference to Table 1 on Page 14 of Applicants' specification. Applicants submit that the specification is double-spaced and that Table 1 on Page 14 complies with 37 C.F.R. § 1.58(c) regarding chemical and mathematical formulae and tables.

### Rejections Under 35 U.S.C. § 112, Second Paragraph

The Examiner rejected claims 3, 6, 14, 15, and 25 under 35 U.S.C. § 112, second paragraph, as allegedly being indefinite. (Paper No. 9 at pages 2-4). The Examiner contended that claims 3, 14, and 25 lack an element directed to "making

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correct allele calls.” (Paper No. 9 at page 3). Applicants have amended those claims to recite “making a correct allele call” (claims 3 and 25) or “make a correct allele call” (claim 14).

The Examiner further contended that claims 3, 14, and 25 are confusing by not reciting what defines the “correct allele call.” *Id.* Applicants have amended those claims to recite making the correct allele call for the signal “based on the determined complexity for the signal.” Support for these amendments can be found, e.g., on page 14, line 7, to page 15, line 9 of Applicants’ specification.

The Examiner further contended that the term “complexity” in claims 3, 14, and 25 is vague and indefinite. *Id.* Applicants point out that breadth of a claim is not to be equated with indefiniteness. MPEP 2173.04 (citing In re Miller, 441 F.2d 689 (CCPA 1971)). As long as one skilled in the art would understand what is claimed, the claim is not indefinite. Applicants assert that one skilled in the art would know the meaning of the term “complexity” in claims 3, 14, and 25 based on at least page 14, line 7, to page 15, line 9 of Applicants’ specification. Therefore, the use of the term “complexity” in claims 3, 14, and 25 is not indefinite.

The Examiner also contended that the phrase “nucleic acid information is nucleic acid length” in claims 6, 15, and 28 is vague and indefinite. (Paper No. 9 at pages 3-4). Specifically, the Examiner indicates that making a correct allele call requires at least panel determination and energy computation information. *Id.* Although Applicants disagree with the Examiner’s contention and solely to advance prosecution, Applicants have amended claims 6, 15, and 28 to encompass certain embodiments of the invention in which the signal representing nucleic acid information is used to determine nucleic

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acid length, panel determination, and energy computation information. Support for these amendments can be found, e.g., on page 14, line 1, to page 16, line 3 of Applicants' specification.

Accordingly, Applicants respectfully request reconsideration and withdrawal of the 35 U.S.C. § 112, second paragraph, rejections.

Claims Rejected Under 35 U.S.C. § 102(b)

The Examiner rejected claims 3, 6, 14, 15, 25, and 28 as allegedly being anticipated by U.S. Patent No. 5,580,728 to Perlin ("Perlin"). (Paper No. 9 at page 4). The Examiner alleged that Perlin teaches all of the elements of these claims. (*Id.* at pages 4-5). Applicants traverse this rejection.

In order to facilitate prosecution and more clearly recite the claimed invention, Applicants amended claims 3, 14, and 25 to recite, *inter alia*, "making" (claims 3 and 25) or "make" (claim 14) a correct allele call for the signal based on the determined complexity for the signal."

To anticipate a claim, the reference must teach each and every limitation of the claim. Claims 3, 14, and 25 recite making or make a correct allele call for the signal *based on the determined complexity for the signal*.

Perlin discusses a method for genotyping using a linear time-to-size interpolation. (Perlin, Col. 8, ll. 24-38). Specifically, Perlin discusses that the method uses a linear time-to-size interpolation to convert the time of each peak apex's occurrence to a DNA size estimate. (Perlin, Col. 12, ll. 53-56). Perlin defines an "apex" as the point of change between a monotonically increasing series and a monotonically decreasing

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series, left to right. (Perlin, Col. 12, ll. 48-51). Thus, the Perlin method fails to teach making a correct allele call based on the determined complexity for the signal, as recited in claims 3, 14, and 25.

Claims 6, 15, and 28 depend from claims 3, 14, and 25, respectively. Because Perlin fails to teach each and every element of claims 3, 14, and 25, as discussed above, it must also fail to teach each and every element of claims 6, 15, and 28. Thus, Applicants need not respond to Examiner's comments under § 102(b) regarding the limitations of those dependent claims. Furthermore, Applicants do not acquiesce in the substantive merits of those comments.

Accordingly, Applicants respectfully request that the Examiner reconsider and withdraw the § 102(b) rejections of claims 3, 5, 14, 15, 25, and 28 over Perlin.

#### Claims Rejected Under 35 U.S.C. § 102(e)

The Examiner rejected claims 3, 6, 14, 15, 25, and 28 as allegedly being anticipated by U.S. Patent No. 6,274,317 to Hiller *et al.* ("Hiller").

Hiller also fails to teach each and every element of claims 3, 14, and 25. In particular, claims 3, 14, and 25 recite making or make a correct allele call *based on the determined complexity for the signal*. This recited claim element is not taught in Hiller.

Hiller discusses an automated allele caller system that applies a typical shape of an allele for a marker to the trace to identify potential allele calls that match the typical shape of the allele at the marker. (Hiller, Abstract, Col. 2, ll. 25-31). Specifically, in Figure 6A, Hiller discusses a method for allele calling that retrieves potential calls and matches a pattern of potential calls to a model shape. (Hiller, Figure 6A, Col. 7, ll. 31-

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42). The Hiller process of allele calling, however, does not teach making a correct allele call based on the determined complexity for the signal, as recited in claims 3, 14, and 25.

Claims 6, 15, and 28 depend from claims 3, 14, and 25, respectively. Because Hiller fails to teach each and every element of claims 3, 14, and 25, as discussed above, it must also fail to teach each and every element of claims 6, 15, and 28. Thus, Applicants need not respond to Examiner's comments under § 102(e) regarding the limitations of those dependent claims. Furthermore, Applicants do not acquiesce in the substantive merits of those comments.

Accordingly, Applicants respectfully request that the Examiner reconsider and withdraw the § 102(e) rejections of claims 3, 6, 14, 15, 25, and 28 over Hiller.

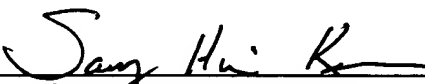
Applicants request the Examiner's reconsideration and reexamination of the application, and the timely allowance of the pending claims. If the Examiner does not agree that the application is in condition for allowance, Applicants request the Examiner to call the undersigned at 650-849-6680 to schedule an interview.

Please grant any extensions of time required to enter this response and charge any additional required fees to Deposit Account No. 06-0916.

Respectfully submitted,

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## APPENDIX

### Specification Amendments

Amendment of paragraph on page 5, lines 4-5:

[Figures 3A-3D depict exemplary allele calling algorithms for use with methods and systems consistent with certain embodiments of the present invention.] Figure 3A depicts an exemplary allele calling algorithm for use with methods and systems consistent with certain embodiments of the present invention.

Figure 3B depicts an exemplary allele calling algorithm for use with methods and systems consistent with certain embodiments of the present invention.

Figure 3C depicts an exemplary allele calling algorithm for use with methods and systems consistent with certain embodiments of the present invention.

Figure 3D depicts an exemplary allele calling algorithm for use with methods and systems consistent with certain embodiments of the present invention.

Please replace the paragraph on page 5, lines 17-18, with the following paragraphs:

[Figures 10 through 12 depict data that can be evaluated with the heuristic algorithm according to certain embodiments.] Figure 10 depicts data that can be evaluated with the heuristic algorithm according to certain embodiments.

Figure 11 depicts data that can be evaluated with the heuristic algorithm according to certain embodiments.

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Figure 12 depicts data that can be evaluated with the heuristic algorithm according to certain embodiments.

#### Claim Amendments

3. (Once amended) A computer-implemented method for making correct allele calls, comprising:
- receiving a signal representing nucleic acid information;
  - determining [whether the signal is below a predefined] a complexity for the signal; and
  - making [an] a correct allele call for the signal based on the [determination] determined complexity for the signal.
6. (Once amended) The method of [any of claims 1, 3, or 4] claim 3, wherein the [nucleic acid information is nucleic acid length] signal is used to determine nucleic acid length, panel determination, and energy computation information.
14. (Once amended) A system for making correct allele calls, comprising:
- a processor configured to execute program instructions; and
  - a memory containing program instructions for execution by the processor to
    - receive a signal representing nucleic acid information,
    - determine [whether the signal is below a predefined] a complexity for the signal, and

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make[an] a correct allele call for the signal based on the  
[determination] determined complexity for the signal.

15. (Once amended) The system of claim 14, wherein the [nucleic acid  
information comprises] the signal is used to determine nucleic acid length, panel  
determination, and energy computation information.

25. (Once amended) A computer-readable medium containing instructions for  
controlling a computer system to perform a method for making correct allele calls, the  
method comprising:

receiving a signal representing nucleic acid information;

determining [whether the signal is below a predefined] a complexity for the  
signal; and

making [an] a correct allele call for the signal based on the [determination]  
determined complexity for the signal.

28. (Once amended) The method of [any of claims 23, 25, or 26] claim 25,  
wherein the [nucleic acid information] signal is used to determine nucleic acid length,  
panel determination, and energy computation information.

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